

Figure S1. Growth of Ura3-HA-degron library isolates in WT versus *doa10*Δ or other E3 ligases implicated in CytoQC. (A-C) Comparing the growth of degron library constructs in WT and *doa10*Δ strains. WT (SM4460) and *doa10*Δ (SM4820) strains transformed with a subset of 77 unique clones isolated in the original degron screen were arrayed in 96-well format, replica-pinned in quadruplicate from solid -Leu media to solid -Leu media (A) and to solid -Leu -Ura media (B, C) and grown for 24 hours. Plates were scanned, and the difference in growth was quantitated and expressed as a heat map (D), in which dark pink, light pink, or white signify a large difference in growth between *doa10*Δ and WT, a small growth difference, or no difference, respectively. Note that Figure S1D is repeated here from Figure 1, for convenience in examining directly together with the actual growth plates. The positions of the 13 representative degrons comprising the “degron tester set” used in later tests are indicated. Controls expressing Ura3p-HA (green boxes), no Ura3p (red boxes), or URA3-HA-CL1 are indicated. Corner positions (yellow boxes) were not used in the analysis. **(E)** Heatmap representation of the relative growth differential for the 77 degron library constructs in strains mutated for the proteasome components Pre1 and Pre2 or E3 ubiquitin ligases known to function in CytoQC, compared to WT strains expressing the same degron. Strains are organized by column, and degrons are organized by rows. Row labels give degron name and its coordinate in 96-well format, corresponding to its location on the growth plates shown in A-D.